

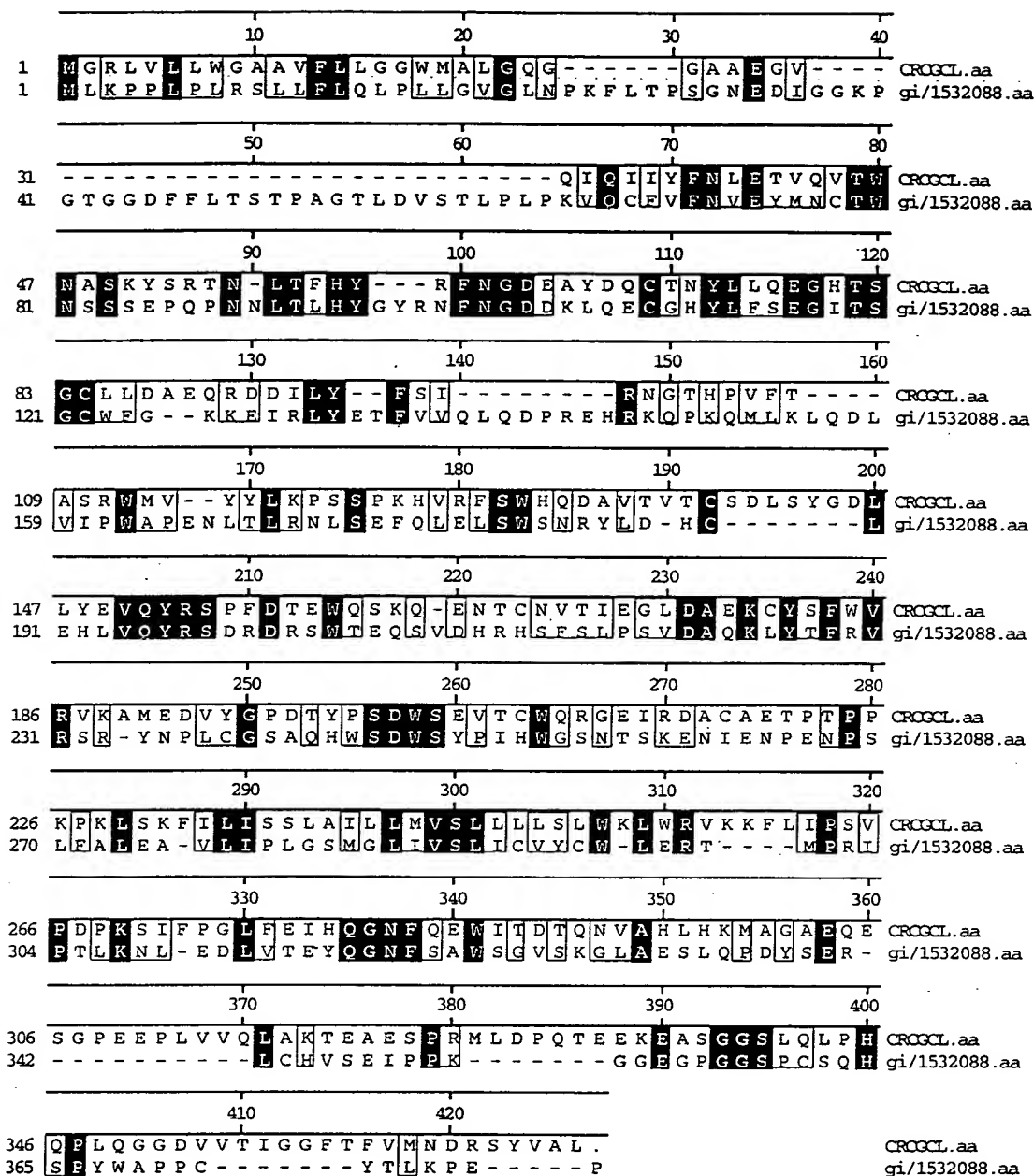
Figure 1A

1	CGGCACGAGGGCATGGGGCGGCTGGTTCTGCTGTGGGGAGCTGCCGTCTTTCTGCTGGGA	60
1	M G R L V L L W G A A V F L L G	16
61	GGCTGGATGGCTTTGGGGCAAGGAGGAGCAGCAGAAGGAGTACAGATTGAGATCATCTAC	120
17	G W M A L G Q G G A A E G V Q I Q I I Y	36
121	TTCAATTTAGAAAACCGTGCGAGGTGACATGGAATGCCAGCAAATACTCCAGGACCAACCTG	180
37	F N L E T V Q V T W N A S K Y S R T N L	56
181	ACTTTCCTACAGATTCAACGGTGATGAGGCCTATGACCAGTGCACCAACTACCTTCTC	240
57	T F H Y R F N G D E A Y D Q C T N Y L L	76
241	CAGGAAGGTCACACTTCGGGGTGCTCCTAGACGCAGAGCAGCGAGACGACATTCTCTAT	300
77	Q E G H T S G C L L D A E Q R D D I L Y	96
301	TTCTCCATCAGGAATGGGACGCACCCCGTTTTCACCGCAAGTCGCTGGATGGTTTATTAC	360
97	F S I R N G T H P V F T A S R W M V Y Y	116
361	CTGAAACCCAGTTCCCGAAGCACGTGAGATTTTCGTGGCATCAGGATGCAGTGACGGTG	420
117	L K P S S P K H V R F S W H Q D A V T V	136
421	ACGTGTCTGACCTGTCTACGGGGATCTCTCTATGAGGTTCAGTACCGGAGCCCTTC	480
137	T C S D L S Y G D L L Y E V Q Y R S P F	156
481	GACACCGAGTGGCAGTCCAAACAGGAAATACCTGCAACGTCAACATAGAAGGCTTGGAT	540
157	D T E W Q S K Q E N T C N V T I E G L D	176
541	GCCGAGAAGTGTTACTCTTTCTGGGTGAGGTGAAGGCTATGGAGGATGTATATGGGCA	600
177	A E K C Y S F W V R V K A M E D V Y G P	196
601	GACACATACCCAAGCGACTGGTCAGAGGTGACATGCTGGCAGAGAGGCGAGATTCCGGAT	660
197	D T Y P S D W S E V T C W Q R G E I R D	216
661	GCCTGTGCAGAGACACCAACGCCTCCCAAACCAAGCTGTCCAAATTTATTTTAATTTCC	720
217	A C A E T P T P P K P K L S K F I L I S	236
721	AGCCTGGCCATCCTTCTGATGGTGTCTCTCTCTCTCTCTCTTTATGGAAATTATGGAGA	780
237	S L A I L L M V S L L L L S L W K L W R	256
781	GTGAAGAAGTTTCTCATTTCCAGCGTGCCAGACCCGAAATCCATCTTCCCCGGGCTCTTT	840
257	V K K F L I P S V P D P K S I F P G L F	276
841	GAGATACACCAAGGGAACCTCCAGGAGTGGATCAGACACCCAGAACGTGGCCCACTC	900
277	E I H Q G N F Q E W I T D T Q N V A H L	296

Figure 1B

901	CACAAGATGGCAGGTGCAGAGCAAGAAAGTGGCCCCGAGGAGCCCTGGTAGTCCAGTTG	960
297	H K M A G A E Q E S G P E E P L V V Q L	316
961	GCCAAGACTGAAGCCGAGTCTCCAGGATGCTGGACCCACAGACCGAGGAGAAAGAGGCC	1020
317	A K T E A E S P R M L D P Q T E E K E A	336
1021	TCTGGGGGATCCCTCCAGCTTCCCCACCAGCCCCCTCCAAGGGGTGATGTGGTCACAATC	1080
337	S G G S L Q L P H Q P L Q G G D V V T I	356
1081	GGGGGCTTCACCTTTGTGATGAATGACCGCTCCTACGTGGCGTTGTGATGGACACACCAC	1140
357	G G F T F V M N D R S Y V A L *	372
1141	TGTCAAAGTCAACGTCAGGATCCACGTTGACATTTAAAGACAGAGGGGACTGTCCCGGGG	1200
1201	ACTCCACACCACCATGGATGGGAAGTCTCCACGCCAATGATGGTAGGACTAGGAGACTCT	1260
1261	GAAGACCCAGCCTCACCGCCTAATGCGGCCACTGCCCTGCTAACTTTCCCCCACATGAGT	1320
1321	CTCTGTGTTCAAAGGCTTGATGGCAGATGGGAGCCAATGCTCCAGGAGATTACTCCCA	1380
1381	GTCCTTTTCGTGCCTGAACGTTGTCACATAAACCCCAAGGCAGCACGTCCAAAATGCTG	1440
1441	TAAAACCATCTTCCCACTCTGTGAGTCCCCAGTTCCGTCCATGTACCTGTTCCATAGCAT	1500
1501	TGGATTCTCGGAGGATTTTGTCTGTTTGTGAGACTCAAACCACTCTACCCCTACAAA	1560
1561	AAAAAAAAAAAAA	1573

Figure 2



Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

Figure 3

